```
### installing required packages to run code -- applies to `%>%` function (used to subset data prior to modeling)
install.packages("dplyr")
require(dplyr)


### First, set the working directory to the folder in which you have stored the companion data file
### this is accomplished using the `setwd` function, for example:

setwd("ADD YOUR FULL WORKING DIRECTORY HERE")


### loading data used to derive BSARs
data <- read.csv("ph_bsar.csv")

### preparing data (subsetting by chemical and species)

lead <- data %>% filter(chemical == "Lead")
other <-  data %>% filter(chemical != "Lead")

splitx <- lapply(split(other, f = other$species, drop = T), FUN = function(x) {
   split(x, f = x$chemical, drop = T)
})


### "smearing" function as per Duan (1983)
### returns average of exponentiated residuals for a model based on log units

smear <- function(x, trans) {
   if(trans == "log" | trans == "ln") {sum(exp(x$residuals))/length(x$residuals)}
   else if(trans == "log10") {sum(10^x$residuals)/length(x$residuals)}
   else {sum(trans^x$residuals)/length(x$residuals)}
}


### calculating correction factors for all models

smear.list <- list()

for (s in 1:length(splitx)){

   smear.list[[s]] <- list()
   length.c <- length(splitx[[s]])

   for(c in 1:length.c){
      smear.list[[s]][[c]] <- smear(lm(log(tiss.lip) ~ log(sed.oc), data = splitx[[s]][[c]]), trans = "log")
      names(smear.list[[s]][[c]]) <- paste(unique(splitx[[s]][[c]]$species), names(splitx[[s]][c]), sep = "-")
   }
}

smears <- round(rbind(cbind(unlist(lapply(smear.list, unlist))),
             "sculpin-lead" = smear(lm(log(tiss.ww) ~ log(sed.dw), data = lead), trans = "log")), 2)
smears ## correction factors
```

note that macoma == field clams

end code
code generated by Brian Church of Windward Environmental LLC on 2/12/2016 at the request of EPA Region 10